IN THE CLAIMS

What is claimed is:

1. **(Currently Amended)** A method of identifying or classifying organisms on a species-specific or taxon-specific level comprising:

   (a) providing a surface plasmon resonance-capable substrate having immobilized thereon one or more species- or taxon-specific nucleic acid probes; then

   (b) contacting the substrate with a sample known to, or suspected of, containing target nucleic acids from an organism to be identified or classified, under conditions and for a time sufficient for sequence-specific hybridization to occur between target nucleic acids present in the sample and the nucleic acid probes immobilized on the substrate, wherein the nucleic acids present in the sample are fragmented before contacting the substrate to the sample; and then

   (c) analyzing the substrate by surface plasmon resonance, whereby sequence-specific hybridization between the target nucleic acids present in the sample and the nucleic acid probes immobilized on the substrate is detected**; and then**

   (d) identifying or classifying the organism from step (b) based upon the specific hybridization detected in step (c).

2. (Original) The method of Claim 1, wherein in step (a) is provided a substrate having a plurality of DNA probes arranged in an array.

3. (Original) The method of Claim 1, wherein in step (a) is provided a substrate having a plurality of RNA probes arranged in an array.

4. (Original) The method of Claim 1, wherein in step (b), the substrate is contacted with a sample containing DNA.

5. (Original) The method of Claim 1, wherein in step (b), the substrate is contacted with a sample containing RNA.

6. (Original) The method of Claim 1, wherein in step (b), the substrate is contacted with a sample containing ribosomal RNA.

7. (Original) The method of Claim 1, wherein in step (c) the substrate is analyzed by surface plasmon resonance imaging.

8. (Previously Cancelled) ~~The method of Claim 1, wherein step (b) further comprises fragmenting the nucleic acids present in the sample before contacting the substrate to the sample.~~

9. (Previously Amended) The method of Claim 1, wherein the nucleic acids present in the sample are fragmented by applying sufficient pressure to the sample to cause nucleic acid fragmentation.

10. (Previously Amended) The method of Claim 1, wherein the nucleic acids present in the sample are fragmented by heating the sample to a sufficient temperature and for a sufficient amount of time to cause nucleic acid fragmentation.

11. **(Currently Amended)** A method of analyzing expression of a gene of interest comprising:

(a) providing a surface plasmon resonance-capable substrate having immobilized thereon one or more nucleic acid probes specifically reactive with mRNA or cDNA corresponding to a gene of interest; then

(b) contacting the substrate with a sample known to, or suspected of, containing mRNA or cDNA corresponding to the gene of interest, under conditions and for a time sufficient for sequence-specific hybridization to occur between the mRNA or cDNA present in the sample and the nucleic acid probes immobilized on the substrate; and then

(c) analyzing the substrate by surface plasmon resonance, ~~whereby~~ **to detect** sequence-specific hybridization between mRNA or cDNA present in the sample and the nucleic acid probes immobilized on the substrate; ~~is detected~~ **and then**

(d) determining timing of expression of the gene of interest, amount of the gene of interest expressed, or physiological location of the expression of the gene of interest based upon the sequence-specific hybridization detected in step (c).

12. (Original) The method of Claim 11, wherein in step (a) is provided a substrate having a plurality of DNA probes arranged in an array.

13. (Original) The method of Claim 11, wherein in step (a) is provided a substrate having a plurality of RNA probes arranged in an array.

14. (Original) The method of Claim 11, wherein in step (b), the substrate is contacted with a sample containing cDNA.

15. (Original) The method of Claim 11, wherein in step (b), the substrate is contacted with a sample containing mRNA.

16. (Original) The method of Claim 11, wherein in step (c) the substrate is analyzed by surface plasmon resonance imaging.

17. (Previously Amended) The method of Claim 11, wherein step (b) further comprises boiling the sample for a period of time sufficient to denature the mRNA or cDNA present in the sample before contacting the substrate to the sample.

18. (Original) The method of Claim 11, wherein step (b) further comprises fragmenting the mRNA or cDNA present in the sample before contacting the substrate to the sample.

19. (Original) The method of Claim 18, wherein the nucleic acids present in the sample are fragmented by applying sufficient pressure to the sample to cause nucleic acid fragmentation.

20. (Original) The method of Claim 18, wherein the nucleic acids present in the sample are fragmented by heating the sample to a sufficient temperature and for a sufficient amount of time to cause nucleic acid fragmentation.

21. (Original) A method of detecting and quantifying sequence-specific hybridization of nucleic acids comprising:

(a) depositing an ω-modified alkanethiol monolayer on a metal substrate;

(b) reacting hydrophobic protecting groups with the monolayer;

(c) patterning the monolayer to create an array of exposed metal substrate areas;

(d) depositing ω-modified alkanethiol in the areas of exposed metal substrate, thereby yielding an array of discrete, unprotected ω-modified alkanethiol spots;

(e) attaching nucleic acid probes to the discrete, unprotected ω-modified alkanethiol spots, thereby yielding an array of discrete spots having nucleic acid probes immobilized thereon;

(f) removing the protecting groups of step (b); and

(g) making the monolayer resistant to non-specific protein binding; and then

(h) contacting the substrate of step (g) with a sample known to, or suspected of, containing target nucleic acids at a concentration not greater than 500 nM, under conditions and for a time sufficient for sequence-specific hybridization to occur between target nucleic acids present in the sample and the nucleic acid probes immobilized on the substrate; and then

(i) analyzing the substrate by surface plasmon resonance, whereby sequence-specific hybridization between the target nucleic acids present in the sample and the nucleic acid probes immobilized on the substrate is detected.

22. (Original) The method of Claim 21, wherein in step (e), DNA molecules are attached to the discrete, unprotected ω-modified alkanethiol spots.

23. (Original) The method of Claim 21, wherein in step (e), RNA molecules are attached to the discrete, unprotected ω-modified alkanethiol spots.

24. (Original) The method of Claim 21, wherein in step (h), the substrate is contacted with a sample containing DNA.

25. (Original) The method of Claim 21, wherein in step (h), the substrate is contacted with a sample containing RNA.

26. (Original) The method of Claim 21, wherein in step (h), the substrate is contacted with a sample containing ribosomal RNA.

27. (Previously Amended) The method of Claim 21, wherein in step (a), the ω-modified alkanethiol monolayer is deposited on a gold substrate.